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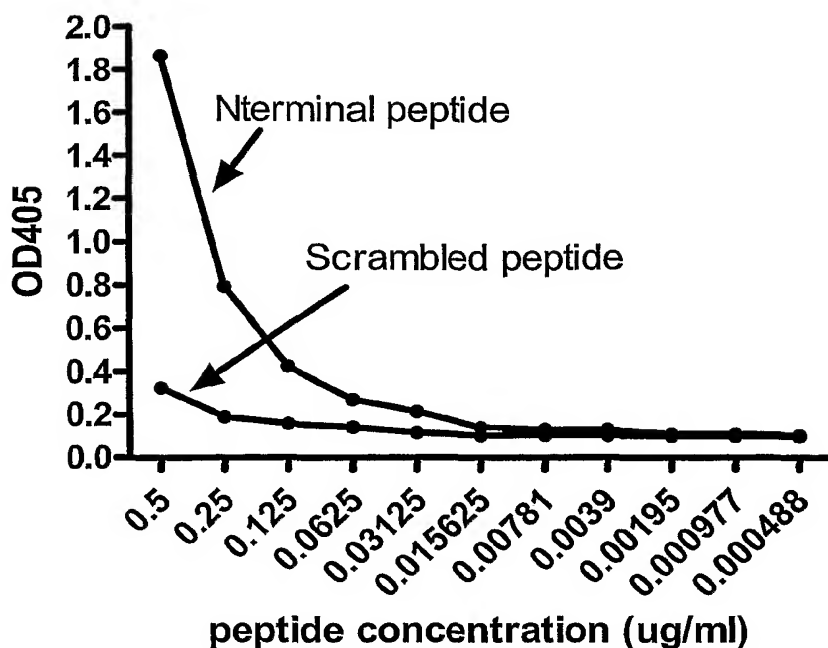
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(54) Title: IDENTIFICATION OF THE PRECISE AMINO ACID SEQUENCE OF THE EPITOPE RECOGNIZED BY THE PO-
TENT NEUTRALIZING HUMAN ANTI-HIV-1 MONOCLONAL ANTIBODY IGG1B12

Peptide binding to IgG1 b12



(57) Abstract: The IgG1b12 human monoclonal antibody binds gp120 strongly, and is the most potent HIV neutralizing antibody known. The exact amino acid sequence of this binding site is not known. We identified the minimal parts of the HIV-1 gp120 (envelope) protein, which IgG1b12 binds to. We did this by quadrupole time of flight (QqTOF) mass spectrometry using epitope excision. Epitope excision allows for determination of conformational epitopes. To do this we bound gp120 to IgG1b12, digested off all unbound portions of gp120, and then ran mass spectrometry of the resulting IgG1b12-gp120 peptide complex. The results allow us to determine the exact amino acid sequence involved in IgG1b12-gp120 interaction.



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